

GenCere version 5.1.3
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OM protein - protein search, using sw model

Pub on January 16, 2003, 16 42:17 : Search time 24 seconds
(without alignments)
58,517 Million cell updates/sec

Title: US-09-856-070-17

Perfect score: 64

Sequence: 1 EREKEQMMREKEEL 14

Scoring table: H05NM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : FIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	581	2 145889	ezrin bovine
2	69	100.0	586	1 A34400	ezrin [validated]
3	69	100.0	630	2 147177	hypothetical prote
4	66	95.7	586	1 B41129	ezrin - mouse
5	51	73.9	577	1 A41289	moesin - human
6	51	73.9	577	1 S39804	moesin - pig
7	51	73.9	583	1 A46127	radixin - human
8	51	73.9	583	1 S39805	radixin - pig
9	51	73.9	583	1 A41129	radixin - mouse
10	51	73.9	451	2 T16624	hypothetical prote
11	47	68.1	1549	1 A40691	trichobyalin - she
12	45	65.2	365	2 T28184	hypothetical prote
13	44	63.8	166	2 T29620	hypothetical prote
14	44	63.8	406	2 T46674	hypothetical prote
15	44	63.8	555	2 T29667	unknown protein, 7
16	44	63.8	2962	2 T19756	hypothetical prote
17	43	62.3	86	2 H69809	hypothetical prote
18	43	62.3	229	2 T23370	conserved hypotet
19	43	62.3	233	2 T17218	hypothetical prote
20	43	62.3	547	2 T40314	hypothetical coile
21	43	62.3	743	2 A29232	18K malaria infi
22	43	62.3	813	2 T02672	hypothetical prote
23	43	62.3	1444	2 T42637	hypothetical prote
24	43	62.3	1407	1 S38589	trichobyalin - lab
25	43	62.3	1898	1 A45973	trichobyalin - hum
26	42	60.9	123	2 B81691	ribosomal-binding f
27	42	60.9	123	2 B81851	ribosomal-binding
28	42	60.9	216	2 T64804	probable membrane
29	42	60.9	420	2 T67229	vitamin D receptor

30	42	60.9	453	2 T42438	mitochondrial proc
31	42	60.9	457	2 T50402	probable mitochond
32	42	60.9	471	1 S62590	peptidyl prol-yl ei
33	42	60.9	525	2 T48824	hypothetical prote
34	42	60.9	580	2 T40867	aspartate-tRNA lig
35	42	60.9	600	2 T51504	hypothetical prote
36	42	60.9	621	2 A57591	Id associated prot
37	42	60.9	849	1 S64732	scalloid attachmen
38	42	60.9	1156	2 T59444	chromosome segrega
39	42	60.9	1378	2 Q88637	protein P5941.4 [i
40	42	60.9	4687	1 A39638	pectin - rat
41	41.5	60.1	220	2 H83967	hypothetical prote
42	41	59.4	85	1 T8BY	g-transferrin AI
43	41	59.4	94	2 S60794	M protein precurs
44	41	59.4	96	2 S60842	M protein precurs
45	41	59.4	235	2 T70405	hypothetical prote

ALIGNMENTS

RESULT 1

145889

ezrin - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 13-Aug-1999

C:Accession: 145889

R:Rerguson, C.M., Zhao, H., Saljuik, K., Duman, R.S., Nestler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A:Title: Ezrin and osteonectin, two proteins associated with cell shape and growth, a

A:Reference number: 145889

A:Accession: 145889

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581; SBR>

A:Cross-references: GB M98498, NID 9289407, PIDN AAA30510.1; FID 9289408

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

F1:291/Domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 100.0%, Score 69, DB 2, Length 581,

Best Local Similarity 100.0%, Pred. No. 0.031;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKEQMMREKEEL 14

DB 334 EREKEQMMREKEEL 347

RESULT 2

A34400

ezrin [validated] - human

N:Alternate names: cyto-villin; p81 protein; villin 2

C:Species: Homo sapiens (man)

C>Date: 30 Jul 1995 #sequence_revision 14 Jul 1994 #text_change 28-Feb 2000

C:Accession: A34400; S09263; E61002

E:Turunen, O.; Winiwiler, R.; Pakkanen, R.; Grzeschik, K.H.; Wahlstrom, T.; Vaheri, A.

J. Biol. Chem. 264, 16727-16732, 1989

A:Title: Cyto-villin, a cytofilin-like protein, cDNA sequence, prokaryotic exp

A:Reference number: A34400; MUID:89380299; PMID:2574140

A:Accession: A34400

A:Molecule type: mRNA

A:Residues: 1-586; TUP>

A:Cross-references: GB S05021

A:Note: the translation of residues 1-11 is not given

A:Note: parts of this sequence were confirmed by protein sequencing

E:Good, K.L.; Friescher, A.; Esch, F.S.; Hunter, T.

EMBO J. 8, 4133-4142, 1989

A:Title: cDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin,

A:Reference number: S05263; MUID:90576135; PMID:2591371

A:Accession: S05263

A:Molecule type: mRNA

A:Residues: 2566-5302

A:Cross-references: GB X51521, NID 931582, FIDN AAA35873.1, FID 931583

R:Banw, G.; Rasmussen, H.H.; Van den Buijck, M.; Van Lomme, J.; Fuyper, M.; Gesset, B.; Electrophoresis 11, 528-536, 1990
 A:Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing
 A:Reference number: A61002; MIM:91041404; PMID:1600755
 A:Accession: E61002
 A:Molecule type: protein
 A:Residues: 255-263; 194, 195, 196, 199, 201, 264, 270, 284-285
 A:Note: it is not certain whether this material represents ezrin or radixin (see entry A61002)
 A:Comment: This material corresponds to transformed epithelial amnion cell (AMA) database
 C:Comment: This protein is located in microvilli and is proposed to play a role in modulating cell motility
 C:Genetics:
 A:Gene: GDB:V112
 A:Cross-references: GDB:120489; OMIM:129000
 A:Map position: 6q25-6q26
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; membrane associated protein, phosphoprotein
 F:2-586/Product: ezrin #status experimental <MAT>
 F:7-291/Domain: protein 4.1 membrane binding domain homology <B41>
 F:553-586/Region: actin binding #status predicted
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted
 F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 69; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred No. 0.042; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 344 EREKQMMREKEEL 347

RESULT 3
 T47177
 hypothetical protein DKFp762H157.1 human (fragment)
 C:Species: homo sapiens (man)
 C:Date: 20 Apr 2000 #sequence_revision 20 Apr 2000 #text_change 02-Sep-2000
 C:Accession: T47177
 Submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24377
 A:Accession: T47177
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-630 <AAA>
 A:Cross-references: EMBL:AL162086
 A:Experimental source: adult melanoma (MeWo cell line); clone DKFp762H157
 C:Genetics:
 A:Note: DKFp762H157.1
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

Query Match 100.0%; Score 69; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred No. 0.044; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 378 EREKQMMREKEEL 391

RESULT 4
 H41129
 ezrin - mouse
 N:Alternate names: cytokerillin; p81 protein; radixin; villin 2
 C:Species: Mus musculus (house mouse)
 C:Date: 03 Aug 1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
 C:Accession: H41129; A46501; A46501; S24203
 R:Funayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.; J. Cell Biol. 115, 1039-1048, 1991
 A:Title: Radixin is a novel member of the band 4.1 family.
 A:Reference number: A41129; MIM:92064645; PMID:1955455
 A:Accession: H41129
 A:Molecule type: mRNA
 A:Residues: 1-586 <FUN>

A:Cross-references: EMBL:X00071; MIM:950880; PIDD:CA443086.1; PIDD:q50881
 R:Garcia, M.; Burgess, W.H.; Chen, B.; Drucker, B.J.; Bretscher, A.; Samelson, L.E.; J. Immunol. 149, 1847-1852, 1992
 A:Title: Identification of ezrin as an 81 kDa tyrosine phosphorylated protein in T cell
 A:Reference number: A46501; MIM:92388649; PMID:1381489
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 412-425 <EGE>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112936)
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-33; 412-425
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112936)
 A:Accession: A46501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 53-57; 148, 149, 150, 151, 152-155 <EG3>
 A:Experimental source: MRL lpr/lpr, T-cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:112940)
 C:Comment: This protein is located in microvilli and is proposed to play a role in microvilli formation
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; ezrin; membrane-associated protein; phosphoprotein
 F:2-586/Product: ezrin #status predicted <MAT>
 F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:553-586/Region: actin binding #status predicted
 F:66/Binding site: phosphate (Ser) (covalent) #status predicted
 F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 95.7%; Score 66; DB 1; Length 586;
 Best Local Similarity 92.4%; Pred No. 0.081; Mismatches 1; Indels 0; Gaps 0;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||
 DB 334 EREKQMMREKEEL 347

RESULT 5
 moesin - human
 N:Alternate names: membrane-organizing extension spike protein
 C:Species: homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A41289
 R:Jankes, W.T.; Farthmayr, H.; Proc. Natl. Acad. Sci. U.S.A. 88, 8297-8301, 1991
 A:Title: Moesin, a member of the protein 4.1-calnexin family of proteins.
 A:Reference number: A41289; MIM:92030840; PMID:1924289
 A:Accession: A41289
 A:Molecule type: mRNA
 A:Residues: 1-577 <LAN>
 A:Cross-references: GDB:M90905; MIM:92030840; PIDD:q188626
 C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma membrane
 C:Genetics:
 A:Gene: GDB:MSN
 A:Cross-references: GDB:136819; OMIM:309845
 A:Map position: Xq11.2-Xq12
 C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
 C:Keywords: actin binding; cytoskeleton; membrane protein
 F:2-577/Product: moesin #status predicted <MAT>
 F:7-291/Domain: protein 4.1 membrane binding domain homology <B41>
 F:544-577/Region: actin binding #status predicted

Query Match 73.9%; Score 51; DB 1; Length 577;
 Best Local Similarity 71.4%; Pred. No. 9.1; Mismatches 3; Indels 1; Gaps 0;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
 |||||

Db 334 EKEKEIEPEKEEL 347

RESULT 6

S39804

moesin - pig

N:Alternate names: membrane-organizing extension spike protein

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jan-1999

C:Accession: S39804

R:Linkes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.

Biochim. Biophys. Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of

F:7-291/Domain: protein 4.1 membrane-binding domain homology

A:Reference number: S39804, MUID:94092743, PMID:8268231

A:Accession: S39804

A:Molecule type: mRNA

A:Residues: 1-577

A:Cross-references: EMBL:M86444; NIH:q14545; PDB:1LQ23

C:Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton; membrane protein

F:2-577/Product: moesin #status predicted <MAT>

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:544-577/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 577;

Best Local Similarity 71.4%; Pred. No. 9.1;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKEIEPEKEEL 347

RESULT 7

A46127

radixin - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jan-1999

C:Accession: A46127

R:Wilgombos, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.

Genomics 16, 199-206, 1993

A:Title: Multicatal cloning, cDNA sequence, and chromosomal assignment of the human radixin

A:Reference number: A46127; NCBI:9302378; PMID:8486157

A:Accession: A46127

A:Molecule type: mRNA

A:Residues: 1-583

A:Cross-references: GR:102320; NIH:q307365; PDB:AAA36541.1; PDB:q307366

A:Note: sequence extracted from NCBI backbone (NCBI:131481, NCBI:131482)

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it is

C:Genetics:

A:Gene: GBR:RDX

A:Cross-references: GR:136270; OMIM:170410

A:Map position: 11q23-11q23

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred. No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKEIEPEKEEL 347

RESULT 8

S39805

radixin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jan-1999

C:Accession: S39805

R:Linkes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.

Biochim. Biophys. Acta 1216, 479-482, 1993

A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification

A:Reference number: S39804, MUID:94092743, PMID:8268231

A:Accession: S39805

A:Molecule type: mRNA

A:Residues: 1-583

A:Cross-references: GR:M86444; EMBL:M86391; NIH:q14545; PDB:AAA2805.1; PDB:q14546

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred. No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKEIEPEKEEL 347

RESULT 9

A41129

radixin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 05-Sep-1997

C:Accession: A41129; S24201

R:Furuyama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.

J. Cell Biol. 115, 1039-1048, 1991

A:Title: Radixin is a novel member of the band 4.1 family.

A:Reference number: A41129; MUID:92064635, PMID:1955455

A:Accession: A41129

A:Molecule type: mRNA

A:Residues: 1-683

A:Cross-references: EMBL:X69672; NIH:q1033049; PDB:q1334260

A:Note: part of this sequence was confirmed by protein sequencing

C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it

C:Superfamily: ezrin, protein 4.1 membrane-binding domain homology

C:Keywords: actin binding; cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>

F:470-477/Region: proline-rich

F:550-583/Region: actin binding #status predicted

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4%; Pred. No. 9.2;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

Db 334 EKEKEIEPEKEEL 347

RESULT 10

T15624

hypothetical protein C25H3.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15624

R:Johnson, D.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid C25H3.

A:Reference number: Z18379

A:Accession: T15624

A:Status: preliminary; translated from GR/EMBL/DDRJ

A:Molecule type: DNA

A:Residues: 1-651

A:Cross-references: EMBL:U02955; NIH:q988451; PDB:q988451

A:Experimental source: strain Bristol N2

C:Genetics:
 A:Gene: CESP:C25H3.6
 A:Introns: 58/71, 213/23, 273/31, 438/2, 478/2, 510/21, 552/33, 607/77

Query Match 73.9% Score 51; DB 2; Length 651;
 Best Local Similarity 84.3% Pred. No. 10;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMKEKE 12
 |||||:|||||
 DB 335 EREKQMMKEKE 346

RESULT 11
 A40691
 Trichohyalin - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 21-Sep-1993 #sequence_revision 0; 01-Mar-1996 #text_change 22-Jun-1999
 C:Accession: A40691; A34209; S32633
 R:Fietz, M.J.; McCaughlan, C.J.; Campbell, M.T.; Rogers, G.E.
 J. Cell Biol. 121, 855-865, 1993
 A:Title: Analysis of the sheep trichohyalin gene: potential structural and calcium-binding
 A:Reference number: A40691; MUID:93260018; PMID:7684041
 A:Accession: A40691
 A:Molecule type: DNA
 A:Residues: 1-1549 <FIE>
 A:Cross-references: EMBL:Z18361; NID:q295940; PIDN:CAA79165.1; PID:q295941
 A:Note: Sequence extracted from NCHI backbone (NCHI:P:132511)
 R:Fietz, M.J.; Presland, R.H.; Rogers, G.E.
 J. Cell Biol. 110, 427-436, 1990
 A:Title: The cDNA-deduced amino acid sequence for trichohyalin, a differentiation marker
 A:Reference number: A34209; MUID:90130532; PMID:2298812
 A:Accession: A34209
 A:Molecule type: mRNA
 A:Residues: 1016-1151, 1295-1359, 1391-1396, 1400-1549 <FIE>
 A:Cross-references: GB:X51695; NID:q1827; PIDN:CAA35992.1; PID:q1828
 C:Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root sheath
 covalent modifications to this protein include conversion of arginine to citrulline and
 C:Genetics:
 A:Introns: 46/3
 A:Note: single copy gene
 C:Superfamily: trichohyalin; calmodulin repeat homology
 C:Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
 F:49-81/Domain: calmodulin repeat homology <EF>
 F:187-851/Region: 28-residue repeats
 F:1886-1519/Region: 23 residue repeats

Query Match 68.1% Score 47; DB 1; Length 1549;
 Best Local Similarity 61.5% Pred. No. 84;
 Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 EREKQMMKEKEEL 14
 |||||:|||||
 DB 1172 EREKQMMKEKEEL 1184

RESULT 12
 T28184
 Hypothetical protein ORF23 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)
 N:Alternate names: ORF MSV024; AL1 motif gene family protein
 C:Species: Melanoplus sanguinipes entomopoxvirus
 C:Variety: isolate Tuscon
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 23-Jul-2000
 C:Accession: T28184
 R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, C.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
 A:Reference number: 220484; MUID:q9102612; PMID:9447359
 A:Accession: T28184
 A:Status: preliminary; translated from GH/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-365 <AFD>
 A:Cross-references: EMBL:AF063866; NID:q4049647; PIDN:AA97848.1; PID:q4049688

A:Experimental source: isolate Tuscon
 C:Genetics:
 A:Note: MSV023

Query Match 65.2% Score 45; DB 2; Length 465;
 Best Local Similarity 61.5% Pred. No. 39;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EREKQMMKEKEEL 14
 |||||:|||||
 DB 114 EREKQMMKEKEEL 126

RESULT 13
 I39620
 Hypothetical protein SPBCL6H5.15 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Nov-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: I39620
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skellion, J.; Chutcher, C.M.
 submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21843
 A:Accession: I39620
 A:Status: preliminary; translated from GR/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-165 <WDS>
 A:Cross-references: EMBL:AL022104; PIDN:CAH60139.1; GSPDB:GN03067; SPDB:SPBCL6H5.15
 A:Experimental source: strain 972h-; cosmid c16H5
 C:Genetics:
 A:Gene: SPDB:SPBCL6H5.15
 A:Map position: 2

Query Match 63.8% Score 44; DB 2; Length 166;
 Best Local Similarity 58.3% Pred. No. 25;
 Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMKEKE 12
 |||||:|||||
 DB 80 KKEKQMMKEKE 91

RESULT 14
 F96679
 Hypothetical protein F5114.2 [imported] Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F96679
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Ansen, N.F.; Hughes, B.; Huizlar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiz, R.; Matz,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96679
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <STO>
 A:Cross-references: GR:Arabidopsis; NID:q2190549; PIDN:AA95093.1; GSPDB:GH00141
 C:Genetics:
 A:Gene: F5114.2
 A:Map position: 1

Query Match 63.8% Score 44; DB 2; Length 406;
 Best Local Similarity 69.2% Pred. No. 59;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EREKQMMKEKE 13
 |||||:|||||

Db 311 ESEKQMKREKEE 323

RESULT 15

C96667

unknown protein, 71502-69704 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02 Mar 2001 #sequence_revision 02 Mar 2001 #text_change 31 Mar 2001

C:Accession: C96667

R:Theologis, A.; Ecker, T.P.; Palm, C.T.; Federspiel, N.A.; Kaul, S.; White, G.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Ansden, N.F.; Hughes, B.; Huizar, L.

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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: AB6141; MUID:21016719; PMID:11130712

A:Accession: C96667

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-555 <SIO>

A:Cross-references: CR AK005173, NID:gl0645451, FUN:AA021515.1; GSPDR:GN00141

C:Genetics:

A:Gene: F15H21.4

A:Map position: 1

Query Match 63.8%; Score 44; DB 2; Length 555;

Best Local Similarity 50.0%; Pred. No. 80;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Caps 0;

QY 1 EREKQMKREKEE 14

DB 473 ANAKDEMAKREKEV 486

Search completed: January 16, 2003, 16:57:47
Job time : 24 secs

